PATENT

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

Applicant:	Walter Keith Jones		
Serial No.:	10/596,516	Group Art Unit:	1632
Filed:	December 16, 2008	Examiner:	Shen, Wu Cheng Winston
For:	**Oligonucleotide Decoys and Methods of Use**		

Mail Stop RCE
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. 1.132

Dr. W. Keith Jones declares that:

1. I am the inventor of and I am familiar with the present application Serial No. 10/596,516, filed on December 16, 2008, and I am familiar with the Office Action dated November 14, 2011 (11-14-11 OA).

2. I have reviewed the references cited in the 11-14-11 OA, particularly Sharma et al., *Transcription factor decoy approach to decipher the role of NF-kappaB oncogenesis*, Anticancer Research 16(1): 61-69 (1996) (hereafter, "Sharma"); Dzau et al., U.S. 2003/0186922, published October 2, 2003 (hereafter, "Dzau"); and Weintraub et al., *Retinoblastoma protein switches the E2F site from positive to negative element*, Nature 358(6383):259-61 (1992) (hereafter, "Weintraub").

3. The Sharma oligonucleotide has the following sequence:

ggggactttccgctggggactttccaggggactttcc

In this sequence, the three NF-kB binding sites are underlined. Using the Basic Local Alignment Search Tool, or BLAST® (available from the National Center for Biotechnology Information, or NCBI), I compared Sharma's sequence to the sequence database and determined that Sharma's oligonucleotide was adapted from the HIV long terminal repeat (LTR) known to have transcription factor activity for NF-kB, by simple addition of a restriction site to one end of the sequence.

4. I also used MATCH™, a weight matrix-based tool for searching putative transcription factor binding sites in DNA sequences (closely interconnected and distributed together with the TRANSFAC® database, available through BIOBASE Biological Databases), to analyze the hypothetical sequence that would result from forming a concatemer with multiple copies of the Sharma oligonucleotide joined end-to-end. MATCH™ results showed that if the Sharma oligonucleotide were concatemerized in this way, the new joint between the copies of the oligonucleotide would introduce new binding sites for Stat 1/3 and Stat 5/6.

5. The Weintraub oligonucleotide has the following sequence:

agcttgttttcgcgcttaaatttgagaaagggcgcgaaactagtca

In this sequence, the two E2F binding sites are underlined. Using BLAST®, I compared Weintraub's sequence to the sequence database and determined that Weintraub's oligonucleotide was derived from the Rous sarcoma virus terminal repeat, which acts as a promoter for the virus. Using MATCH™, I determined that the Weintraub oligonucleotide also has a binding site for

Pax-6 (grey box) which overlaps with one E2F site and a biding site for CP2 (white box), which overlaps with the other E2F site.

6. I also used MATCH™ to analyze the hypothetical sequence that would result from forming a concatemer with multiple copies of the Weintraub oligonucleotide joined end-to-end. MATCH™ results showed that if the Weintraub oligonucleotide were concatemerized in this way, the new joint between the copies of the oligonucleotide would introduce new binding sites for GCN4, Jun B/D, and Opaque-2.

7. All statements made herein of my own knowledge are true and all statements made on information and belief are believed to be true; these statements were made with the knowledge that willful and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,

5-11-12
Date

W. Keith Jones
Dr. W. Keith Jones